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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/786,475	KONVICKA, KAREL	
	Examiner	Art Unit	
	Russell S. Negin	1631	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *18 July 2007*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-79* is/are pending in the application.

4a) Of the above claim(s) *14,15,19,78 and 79* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-13,16-18 and 20-77* is/are rejected.

7)☒ Claim(s) *17* is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Comments

Applicants' amendments and request for reconsideration in the communication filed on 18 July 2007 are acknowledged and the amendments are entered.

Claims 1-79 are pending, and claims 1-13, 16-18, and 20-77 are examined in this Office action.

Claim Objections

The following objection is newly applied:

Claim 17 is objected to because of the following informalities:

The phrase, "comprising carrying out a first K-means algorithm 10 and a second K-menas algorithm," needs grammatical clarification (the purpose of the number 10 is not understood).

Appropriate correction is required.

Claim Rejections - 35 USC § 101

The following rejection is reiterated from the Office action sent on 18 April 2007:

35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claims 1-13, 16-18, and 20-77 are rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter.

The following analysis of facts of this particular patent application follows the analysis suggested in the "Interim Guidelines for Examination of Patent Applications for Patent Subject Matter Eligibility". Note that the text of the Guidelines is italicized.

To satisfy section 101 requirements, the claim must be for a practical application of the § 101 judicial exception, which can be identified in various ways (Guidelines, p. 19):

- The claimed invention "transforms" an article or physical object to a different state or thing.

- The claimed invention otherwise produces a useful, concrete and tangible result.

In the instant case, the claimed invention does not "transform" an article or physical object to a different state or thing because it is a method of determining a genotype of at least one individual. This does not preclude the subject matter to be patentable as, for eligibility analysis, as

physical transformation "is not an invariable requirement, but merely one example of how a mathematical algorithm [or law of nature] may bring about a useful application." AT&T, 172 F.3d at 1358-59, 50 USPQ2d at 1452. If the examiner determines that the claim does not entail the transformation of an article, then the examiner shall review the claim to determine if the claim provides a practical application that produces a useful, tangible and concrete result. In determining whether the claim is for a "practical application," the focus is not on whether the steps taken to achieve a particular result are useful, tangible and concrete, but rather that the final result achieved by the claimed invention is "useful, tangible and concrete." The claim must be examined to see if it includes anything more than a § 101 judicial exception. If the claim is directed to a practical application of the § 101 judicial exception producing a result tied to the physical world that does not preempt the judicial exception, then the claim meets the statutory requirement of 35 U.S.C. § 101.

If the examiner does not find such a practical application, the examiner has determined that the claim is nonstatutory. (Guidelines, p. 20)

The question is thus whether the final result achieved by the claimed invention satisfies all three criteria of being useful, and concrete, and tangible.

Furthermore, the useful, tangible, and concrete result must be recited in the claim itself, rather than addressed in specification.

(2) **"TANGIBLE RESULT"** The tangible requirement does not necessarily mean that a claim must either be tied to a particular machine or apparatus or must operate to change articles or materials to a different state or thing. However, the tangible requirement does require that the claim must recite more than a § 101 judicial exception, in that the process claim must set forth a practical application of that § 101 judicial exception to produce a real-world result. The opposite meaning of "tangible" is "abstract."

The instant claims are drawn to a method for determining the genotype of at least one individual. However, as claimed, the method does not produce a tangible result. For example, the method as claimed may take place entirely within the confines of a computer or a human mind without any communication to the outside world and without using or making available for use, the results of the computation. For example, the genotype can be stored in a carrier wave, which, per se, is not statutory. Thus, the instant methods of the claims do not produce any tangible result.

Therefore, the final result achieved by the claimed invention does not satisfy all three criteria of being useful, and concrete, and tangible.

Response to Arguments:

Applicant's arguments filed 18 July 2007 have been fully considered but they are not persuasive.

Applicant argues the following on page 17 of the Remarks:

> In particular, the process of identifying the genotype of one or more individuals is of particular applicability in the field of molecular biology, as well as all of its research and industrial applications. Identification of the genotype is itself a tangible result, because it represents aspects of the genetic code of the individual, which is not an abstract idea but a tangible physical quality.

This is not persuasive, because while a genotype may have importance in a scientific field, it is a property and not a physical entity. Unless this genotype is displayed in a manner that is tangibly observable (i.e. on a display or sheet of paper), it is not considered a statutory (i.e. the result of the claim is intangible).

The amendments of applicant do not overcome the rejections for the reasons disclosed in the above rejection.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 1-2 and 5-8 are rejected under 35 U.S.C. 102(b) as being anticipated by Clark et al. [Human Genetics, 2001, volume 108, pages 484-493].

Claim 1 is drawn to a method for determining a genotype of at least one individual from a genetic marker using at least one measure of the amount of a given allele of the genetic marker in the individual, comprising:

--assigning the measure of the amount of the allele to a group using one or more of a probability clustering process and a distance clustering process;

--assigning a genotype to the group based on a property of the group, wherein the individual is determined to have the genotype assigned to the group; and

--storing the genotype in a medium accessible to a user.

Claim 2 depends from claim 1 with the additional limitation of being computer implemented.

The study of Clark et al. examines a statistical estimation and pedigree analysis of CCR2-CCR5 haplotypes. Clark et al. states in the abstract:

> As more SNP marker data becomes available, researchers have used haplotypes of markers, rather than individual polymorphisms, for association analysis of candidate genes.

Figure 2 on page 487 of Clark et al. illustrates the cluster analysis, allele determination and SNP analysis as a scatter plot of the 5' nuclease assay output for an SNP (L55Q) in exon 4 of CCR5. The first paragraph under Results on pages 486-487 states with regards to the Figure:

> A scatter plot of the 5' nuclease assay results for CCR5-L55Q is shown in Fig. 2. This plot represents the result of 96 assay reactions, in which genotypes were determined visually in the dye components view of the SDS software.... Four distinct clusters of dots are evident. T/T homozygotes are clustered along the X-axis. A/A homozygotes are clustered along the Y-axis, and the middle cluster corresponds to T/A heterozygotes.

Consequently, Figure 2 of Clark et al. illustrates the genotyping, assignment of allele measures and storage of the results on a computer printout as required by the instant claims.

Claim 5 is dependent from claim 1 with the additional limitation that the individual is a diploid organism.

Claim 6 is dependent from claim 5 with the additional limitation that the diploid organism is a mammal.

Claim 7 is dependent from claim 6 with the additional limitation that the mammal is a human. The "Samples" section of column 1 of page 486 indicates that the specimens were taken from humans.

Claim 8 is dependent from claim 1 with the additional limitation that the probability clustering process carries out an expectation maximization algorithm.

Column 2 on page 486 of Clark et al. (line 16) states "Haplotype estimation was performed by the EM method."

Claim Rejections - 35 USC § 103

The rejection of claims 1-2, 5-7, 63, and 73 under 35 U.S.C. 103(a) as being unpatentable over Lee et al. [Proceedings of the SPIE, 2001, volume 4266, pages 228-235] is withdrawn in view of arguments by applicant on pages 18-20 of the Remarks.

The rejection of claims 1 and 3-4 under 35 U.S.C. 103(a) as being unpatentable over Lee et al. as applied above, and further in view of Xue et al. [PGPUB 2003/0017487] is withdrawn in view of arguments by applicant on pages 18-20 of the Remarks.

The rejection of claims 1, 9-13, 16-18, 20-22, 25, 63, 65, 67-70, 73, 75,and 76 under 35 U.S.C. 103(a) as being unpatentable over Lee et al. as above, and further in view of Krishna et al. [IEEE Transactions of Systems, Man, and Cybernetics—Part B: Cybernetics, volume 29, June 1999, pages 433-439] is withdrawn in view of arguments by applicant on pages 18-20 of the Remarks.

The rejection of claims 1, 8, 63-64, and 73-74 under 35 U.S.C. 103(a) as being unpatentable over Lee et al. as applied above, and further in view of Excoffier et al. [Mol. Biol. Evol. Volume 12, pages 921-927, 1995] is withdrawn in view of arguments by applicant on pages 18-20 of the Remarks.

The rejection of claims 1, 25-53, 63, 65, 73, and 77 under 35 U.S.C. 103(a) as being unpatentable over Lee et al. in view of Krishna et al. as applied above, and further in view of Montoya-Delgado et al. [Genetics, volume 158, pages 875-883, June 2001] in view of Frey et al. [Journal of Immunological Methods, 1998, volume 221, pages 35-41] is withdrawn in view of arguments by applicant on pages 18-20 of the Remarks.

The rejection of claims 58-62, 63, 67, and 69-72 under 35 U.S.C. 103(a) as being unpatentable over Lee et al. in view of Krishna et al. as applied above, and further in view of Excoffier et al. is withdrawn in view of arguments by applicant on pages 18-20 of the Remarks.

The rejection of claims 63 and 66 under 35 U.S.C. 103(a) as being unpatentable over Lee et al. in view of Krishna et al. as applied above, and further in view of Babu et al. [Pattern Recognition Letters, volume 14, 1993, pages 763-769] is withdrawn in view of arguments by applicant on pages 18-20 of the Remarks.

The rejection of claims 1, 26, 38-39, 44, and 54-57 under 35 U.S.C. 103(a) as being unpatentable over Lee et al. in view of Krishna et al. in view of Montoya-Delgado et al. in view of Frey et al. as applied above, and further in view of Babu et al. is withdrawn in view of arguments by applicant on pages 18-20 of the Remarks.

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

35 U.S.C. 103 Rejection #1:

Claims 63-64 and 73-74 are rejected under 35 U.S.C. 103(a) as being unpatentable over Clark et al. as applied to claims 1-2, and 5-8 above.

Claim 63 is drawn to all of the limitations of claim 1 except it is on a data processing apparatus instead of as a method.

Claim 64 is dependent from claim 63 with the additional limitation of incorporating an expectation maximization algorithm.

Claim 73 is drawn to all of the limitations of claim 1 except it is on a computer readable medium instead of as a method.

Claim 74 is dependent from claim 73 with the additional limitation of incorporating an expectation maximization algorithm.

The study of Clark et al. examines a statistical estimation and pedigree analysis of CCR2-CCR5 haplotypes. Clark et al. states in the abstract:

> As more SNP marker data becomes available, researchers have used haplotypes of markers, rather than individual polymorphisms, for association analysis of candidate genes.

Figure 2 on page 487 of Clark et al. illustrates the cluster analysis, allele determination and SNP analysis as a scatter plot of the 5' nuclease assay output for an

SNP (L55Q) in exon 4 of CCR5. The first paragraph under Results on pages 486-487 states with regards to the Figure:

> A scatter plot of the 5' nuclease assay results for CCR5-L55Q is shown in Fig. 2. This plot represents the result of 96 assay reactions, in which genotypes were determined visually in the dye components view of the SDS software.... Four distinct clusters of dots are evident. T/T homozygotes are clustered along the X-axis. A/A homozygotes are clustered along the Y-axis, and the middle cluster corresponds to T/A heterozygotes.

Consequently, Figure 2 of Clark et al. illustrates the genotyping, assignment of allele measures and storage of the results on a computer printout as required by the instant claims.

Column 2 on page 486 of Clark et al. (line 16) states "Haplotype estimation was performed by the EM method."

Clark et al. as applied to claims 1-2 and 5-8 above does not disclose the use of a computer apparatus or a computer readable media. However, according to the court decision of In re Venner:

> In re Venner, 262 F.2d 91, 95, 120 USPQ 193, 194 (CCPA 1958) (Appellant argued that claims to a permanent mold casting apparatus for molding trunk pistons were allowable over the prior art because the claimed invention combined "old permanent-mold structures together with a timer and solenoid which automatically actuates the known pressure valve system to release the inner core after a predetermined time has elapsed." The court held that broadly providing an automatic or mechanical means to replace a manual activity which accomplished the same result is not sufficient to distinguish over the prior art.).

Consequently, it is obvious to someone of ordinary skill in the art to automate the manual activity of Clark et al. as applied to claims 1-2 and 5-8 above to result in a more expedient, and accurate process.

35 U.S.C. 103 Rejection #2:

Claim 4 is rejected under 35 U.S.C. 103(a) as being unpatentable over Clark et al. as applied to claims 1-2, 5-8, 63-64, and 73-74 above, and further in view of Xue et al. [PGPUB 2003/0017487].

Clark et al. as applied to claims 1-2, 5-8, 63-64, and 73-74 above fail to teach the method of finding markers (SNPs) to determine genotypes, and they fail to teach such analyses for haploid organisms.

Xue et al. in Figure 2 does teach SNP analysis of haploid cells.

The purpose of the study of Xue et al. is taught in paragraph [0005]:

> In order to screen a large number of different samples, there is a need for a method with improved efficiency. It is therefore an object of the present invention to provide a novel method for scoring single nucleotide polymorphism.

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify Clark et al. as applied to claims 1-2, 5-8, 63-64, and 73-74 above further view of Xue et al. because Xue et al. has the advantage of being a method of screening cells with increased efficiency for SNPs.

35 U.S.C. 103 Rejection #3:

Claims 9-12, 20-22, 58-60, 65, 67-70, 72, 75, and 76 are rejected under 35 U.S.C. 103(a) as being unpatentable over Clark et al. as applied to claims 1-2, 5-8, 63-64, and 73-74 above, and further in view of Krishna et al. [IEEE Transactions of Systems, Man, and Cybernetics—Part B: Cybernetics, volume 29, June 1999, pages 433-439].

Claim 9 is dependent from claim 1 with the additional limitation that the distance based clustering process carries out at least one K means algorithm.

Claim 10 is dependent from claim 1 with the additional limitation that the at least one K-means algorithm is initiated by assigning a plurality of mean values distributed from about 0 to about 1.

Claim 11 is dependent from claim 10 with the additional limitation that 10 mean values are assigned.

Clark et al. as applied to claims 1-2, 5-7, 63, and 73 above fail to teach analysis in terms of K-means genetic algorithms.

The article of Krishna et al, entitled, "Genetic K-Means Algorithm," states in its abstract:

> In this paper, we propose a novel hybrid genetic algorithm (GA) that finds a globally optimal partition of a given data into a specified number of clusters. GA's used earlier in clustering employ either an expensive crossover operator to generate valid child chromosomes from parent chromosomes or a costly fitness function or both. To circumvent these expensive operations, we hybridize GA with a classical gradient descent algorithm viz., K-means algorithm. Hence, the name genetic K-means algorithm (GKA). We define K-means operator, one-step of K-means algorithm, and use it in GKA as a search operator instead of crossover. We also define a biased mutation operator specific to clustering called distance-based-mutation. Using finite Markov chain theory, we prove that the GKA converges to the global optimum. It is observed in the simulations that GKA converges to the best known optimum corresponding to the given data in concurrence with the convergence result. It is also observed that GKA searches faster than some of the other evolutionary algorithms used for clustering.

Tables I and II on page 348 of Krishna et al. illustrate the assignation of 10 means with the plurality of mean values distributed between "approximately" 0 and "approximately" 1. Equation 3 on page 434 illustrates a plurality or greater than three centroids or density centers.

The actual K-means algorithm is illustrates on the bottom of column 1 on page 436 of Krishna et al. It can be carried out multiple times until optimization to a solution as it is iterative.

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify Lee et al. as applied to claims 1-2, 5-8, 63-64, and 73-74 above as applied to claims 1-2, 5-8, 63-64, and 73-74 above, and further in view of Krishna et al. because Krishna et al. has the advantage of employing a genetic K means cluster analysis for more expeditious analysis of the data.

Claim 12 is dependent from claim 9 with the additional limitation that each subset comprises three density center values.

Equations 4 and 5 of Krishna et al. on column 2 of page 434 list within-cluster variations and total within cluster variations used to evaluate variances.

Claim 20 is dependent from claim 1 with the additional limitation that the probability clustering process is initiates using a solution obtained by at least one K=means algorithm.

The focus of Krishna et al. is to use K means clustering to analyze biological clustering problems (see abstract).

Claim 21 is dependent from claim 1 with the additional limitation of having a process that yields a certain standard deviation for the distribution.

The equation after equation 5 in column 2 of page 434 shows such a standard deviation.

Claim 22 is dependent from claim 1 with the additional limitation of assigning the amount of an allele using clustering processes. Figure 2 of Clark et al. in combination with the K means clustering process of Krishna et al. illustrates such a probabilistic clustering process.

Claim 58 is drawn to a computer implemented method for determining one or more genotypes of a plurality of individuals at a SNP position using respective measures of a relative allele amount for the SNP position for each individual, comprising:

--assigning the measures of the relative allele amount to a group using one or more of an expectation maximization process and a K-means process;

--assigning a genotype to each group identified by the expectation maximization process and/or the K-means process to determine a genotype of each person;

--assessing a confidence of determination of the genotype; and

--storing the genotype in a medium accessible to a user.

The study of Clark et al. examines a statistical estimation and pedigree analysis of CCR2-CCR5 haplotypes. Clark et al. states in the abstract:

> As more SNP marker data becomes available, researchers have used haplotypes of markers, rather than individual polymorphisms, for association analysis of candidate genes.

Figure 2 on page 487 of Clark et al. illustrates the cluster analysis, allele determination and SNP analysis as a scatter plot of the 5' nuclease assay output for an SNP (L55Q) in exon 4 of CCR5. The first paragraph under Results on pages 486-487 states with regards to the Figure:

> A scatter plot of the 5' nuclease assay results for CCR5-L55Q is shown in Fig. 2. This plot represents the result of 96 assay reactions, in which genotypes were determined visually in the dye components view of the SDS software.... Four distinct clusters of dots are evident. T/T homozygotes are clustered along the X-axis. A/A homozygotes are clustered along the Y-axis, and the middle cluster corresponds to T/A heterozygotes.

Consequently, Figure 2 of Clark et al. illustrates the genotyping, assignment of allele measures and storage of the results on a computer printout as required by the instant claims.

Clark et al. does not teach the use of K-means clustering.

The article of Krishna et al, entitled, "Genetic K-Means Algorithm," states in its abstract:

> In this paper, we propose a novel hybrid genetic algorithm (GA) that finds a globally optimal partition of a given data into a specified number of clusters. GA's used earlier in clustering employ either an expensive crossover operator to generate valid child chromosomes from parent chromosomes or a costly fitness function or both. To circumvent these expensive operations, we hybridize GA with a classical gradient descent algorithm viz., K-means algorithm. Hence, the name genetic K-means algorithm (GKA). We define K-means operator, one-step of K-means algorithm, and use it in GKA as a search operator instead of crossover. We also define a biased mutation operator specific to clustering called distance-based-mutation. Using finite Markov chain theory, we prove that the GKA converges to the global optimum. It is observed in the simulations that GKA converges to the best known optimum corresponding to the given data in concurrence with the convergence result. It is also observed that GKA searches faster than some of the other evolutionary algorithms used for clustering.

The actual K-means algorithm is illustrated on the bottom of column 1 on page 436 of Krishna et al.

Claim 59 is dependent from claim 58 with the additional limitation that the expectation maximization process is initiated using a K-means algorithm.

Claim 60 is dependent from claim 58 with the additional limitation that assessing the confidence includes using a chi-squared distribution to evaluate a spread of at least one of said groups and evaluating whether a distribution of the individuals between the groups conforms to a corresponding Hardy-Weinberg equilibrium distribution.

Column 2 on page 496 of Clark et al. states in lines 10-16:

> Each SNP had two co-dominant alleles. Mendellian transmission in the CEPH families was tested by using the pedigree algorithms implemented in PedCheck.... Allele frequencies in the population samples were determined by direct gene counting. Genotype distributions in each sample were evaluated for departure from Hardy-Weinberg expectation by using a contingency table chi squared test.

Consequently. The combination of the chi squared test, the Hardy Weinberg expectation and the K-means clustering described the instantly rejected claims.

Claim 65 is dependent from claim 63 with the additional limitation that the computer code executing a distance based clustering process carries out at least one K-means algorithm.

The actual K-means algorithm is illustrated on the bottom of column 1 on page 436 of Krishna et al.

Claim 67 is dependent from claim 63 with the additional limitation that the probability clustering process is initiated using a solution obtained by at least one K-means algorithm.

The article of Krishna et al, entitled, "Genetic K-Means Algorithm," states in its abstract:

> In this paper, we propose a novel hybrid genetic algorithm (GA) that finds a globally optimal partition of a given data into a specified number of clusters. GA's used earlier in clustering employ either an expensive crossover operator to generate valid child chromosomes from parent chromosomes or a costly fitness function or both. To circumvent these expensive operations, we hybridize GA with a classical gradient descent algorithm viz., K-means algorithm. Hence, the name genetic K-means algorithm (GKA). We define K-means operator, one-step of K-means algorithm, and use it in GKA as a search operator instead of crossover. We also define a biased mutation operator specific to clustering called distance-based-mutation. Using finite Markov chain theory, we prove that the GKA converges to the global optimum. It is observed in the simulations that GKA converges to the best known optimum corresponding to the given data in concurrence with the convergence result. It is also observed that GKA searches faster than some of the other evolutionary algorithms used for clustering.

The actual K-means algorithm is illustrated on the bottom of column 1 on page 436 of Krishna et al.

Claim 68 is dependent from claim 63 with the additional limitation of using probabilistic clustering and/or distance clustering to yield a standard deviation for at least one amount of an allele.

The equation below equation number 5 in column 2 of page 434 of Krishna et al. illustrates the use of standard deviations to analyze K-means clustering.

Claim 69 is dependent from claim 67 with the additional limitation the computer code executes both a probability and a distance based clustering process.

While Clark et al. teaches a probability clustering process (see abstract), Kriskna et al. teach a K-means clustering analysis (see abstract).

Claim 70 is dependent from claim 69 with the additional limitation the probability clustering process carries out an expectation maximization algorithm and the distance based clustering process carrier out at least one K-means algorithm.

Claim 72 is dependent from claim 63 with the additional limitation of determining the genotype of at least one individual.

While Clark et al. shows the EM algorithm (see methods on page 486), Krishna et al. teaches the use of distance based clustering using a K-means clustering process (see abstract).

Claim 75 is dependent from claim 73 with the additional limitation that the distance based clustering process comprises a K-means algorithm.

Claim 76 is dependent from claim 73 with the additional limitation that the amount of an allele is assigned using both a probability clustering process and a distance clustering process.

While Clark et al. shows the EM algorithm (see methods on page 486), Krishna et al. teaches the use of distance based clustering using a K-means clustering process (see abstract).

35 U.S.C. 103 Rejection #4:

Claims 66 is rejected under 35 U.S.C. 103(a) as being unpatentable over Clark et al. in view of Krishna et al. as applied to claims 9-12, 20-22, 58-60, 65, 67-70, 72, 75, and 76 above, and further in view of Babu et al. [Pattern Recognition Letters, volume 14, 1993, pages 763-769].

Clark et al. in view of Krishna et al. as applied to claims 9-12, 20-22, 58-60, 65, 67-70, 72, 75, and 76 above do not teach K means seeding algorithms.

The article of Babu et al, entitled, "A near optimal initial seed selection in K-means algorithm using a genetic algorithm," states in its abstract, "The K-means algorithm for clustering is very much dependency on the initial seed values. We use a genetic algorithm to find a near optimal partitioning of the given data set by selecting proper initial seed values in the K-means algorithm..."

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify Clark et al. in view of Krishna as applied to claims 9-12, 20-22, 58-60, 65, 67-70, 72, 75, and 76 above, and further in view of Babu et al. because Babu et al. has a systematic means of generating seed values from which the clustering is very much dependent.

Response to Arguments

Applicant's arguments filed 18 July 2007 have been fully considered and they are persuasive. New grounds of rejection are applied.

Conclusion

No claim is allowed.

Papers related to this application may be submitted to Technical Center 1600 by facsimile transmission. Papers should be faxed to Technical Center 1600 via the central PTO Fax Center. The faxing of such pages must conform with the notices published in the Official Gazette, 1096 OG 30 (November 15, 1988), 1156 OG 61 (November 16, 1993), and 1157 OG 94 (December 28, 1993)(See 37 CFR § 1.6(d)). The Central PTO Fax Center Number is (571) 273-8300.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Russell Negin, Ph.D., whose telephone number is (571) 272-1083. The examiner can normally be reached on Monday-Friday from 7am to 4pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's Supervisor, Marjorie Moran, Supervisory Patent Examiner, can be reached at (571) 272-0720.

Information regarding the status of the application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information on the PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

/Shubo (Joe) Zhou/

RSN 9/27/07
27 September 2007

SHUBO (JOE) ZHOU, PH.D.
PRIMARY EXAMINER